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TITLE

Genetic variation of *Echinococcus* species in domestic and wild canines of North Khorasan Province, northeast Iran

Heidari Z [1,2], Kia E.B [1,2], Mobedi I [1], Mirhendi SH [3], Sharbatkhori M [4], Nikmanesh B [5], Sharifdini M [6], Mohebali M [1,2], Zarei Z [1], Arzamani K [7]

1. *Department of Medical Parasitology and Mycology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran*
2. *Center for Research of Endemic Parasites of Iran (CREPI), Tehran University of Medical Sciences, Tehran, Iran*
3. *Department of Medical Mycology and Parasitology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran.*
4. *Laboratory Sciences Research Center, Golestan University of Medical Sciences, Gorgan, Iran.*
5. *Department of Lab Medical Sciences, School of Allied Medical Sciences, Tehran University of Medical Sciences, Tehran, Iran*
6. *Department of Medical Parasitology and Mycology, School of Medicine, Guilan University of Medical Sciences, Rasht, Iran*
7. *Vector-borne Diseases Research Center, North Khorasan University of Medical Sciences, Bojnurd, Iran*

*** Corresponding author:**
keiaeshr@tums.ac.ir

Background: Canids are definitive hosts for *Echinococcus* species, causative agents of echinococcosis. This study aimed to determine genetic variation of *Echinococcus* species in domestic and wild canines of North Khorasan Province, northeast Iran.

Methods: During 2013 and 2014, the carcasses of 106 canines were collected from the study area and examined for infectivity with *Echinococcus* species. DNA from *Echinococcus* samples were extracted using tissue DNA extraction kit. The cox1 and nad1 mitochondrial genes were amplified and sequenced. Alignments of the sequences, comparisons with registered sequences in GenBank, and phylogenetic analysis were performed. Intra-species and inter-species diversity were calculated.

Results: *Echinococcus granulosus* were found in jackal (3.3%), dog (21.1%) and wolf (33.3%). *Echinococcus multilocularis* were found in jackal (13.1%) and fox (8.7%). All isolates of *E. granulosus* identified as G1 genotype. Based on the comparative analysis of *Echinococcus* sequences homology, intra-species genetic diversity for pcox1 and pnad1 within *E. granulosus* isolates were 0-0.7% and none, respectively; and these amounts within *E. multilocularis* isolates were none and 0-0.2%, respectively.

Conclusion: Analysis of pcox1 and pnadl of *Echinococcus* isolates revealed circulation of both *E. granulosus* and *E. multilocularis* in the canids of the study area.

Keywords: genetic variation, *Echinococcus granulosus, Echinococcus multilocularis*, canids, Iran